

Figure 1

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10      20      30      40
1  MA--QQTTLQEENSVYPKLEEAALLDHARSYKLPQEQLDWY G.f.
1  MS--AVDKRAKFESALPVFVDEIVNYLKTINIPDDVTEWY S.p.
1  MA--KTTTTLKEFESVFPKLEEAALLEYAKAYKLPQEQMLSWY N.c.
1  MSDN-----RAQFLEVFVPSLVQELRDILAGYGMPEEAIEWY K.l.
1  MASEKEIRRRERFLNVFPKLVEEELNASLLAYGMPKEACDWY S.c.
1  -----S.p.
1  -----S.m.

50      60      70      80
39 KRSLEVNPLGGKCNRGMSVPSVSLLE--KPLTEEEQY G.f.
39 KNSLFHNTLGGKYNRGLSVIDSYEILLG--HPLDEEAAY S.p.
39 KQSLEVNNTLGGKCNRGMSVPSASILLG--RPLTEEEY N.c.
37 EKSLNYNTPGGKLNRLSVVDTYALLKGYKSVSELSAEEY K.l.
41 AHSNLYNTPGGKLNRLSVVDTYAILSN-KTVEQLGQEEY S.c.
1  -----C.p.
1  -----S.m.

90      100     110     120
75 FQAATLGLWMTEELLQAFFFLVSDDIMDSSI TRRGQPCWYRQE G.f.
75 MKA AVLGLWMVELLQSSFFLIADDIMDASK TRRGQPCWYLM P S.p.
75 FQAATLGLWMTEELLQAFFFLVSDDIMDSSI TRRGKPCWYRQE N.c.
77 KKVAILGLWCIELLQAYFLVADDMMDQSI TRRGQPCWYKVE K.l.
80 EKVAAILGLWCIELLQAYFLVADDMMDKSI TRRGQPCWYKVP S.c.
28 FHAATLGLWMTEELLQAFFELVSDDIMDGSITRRRKPCWHHRQD C.p.
28 FKSATLGLWMTEELLQAFFFLVSDDIMDSSKTRRGSPCWYLM P S.m.

130     140     150     160
115 GVGMI AINDAFMLESAIYTLLKKKYFRSHPAYFDLIESFHE G.f.
115 GVGNI AINDAFMVESAIYFLLKKKHFRQESCYVDLIELEFHE S.p.
115 GVGMI AINDAFMLESAIYTRLKKKYFRSHPRYVDFLELEFHE N.c.
117 NVGDI AINDAFMLEGAIYCLLKKKHFRTEPYVVDLLELEFHE K.l.
120 EVGEI AINDAFMLEAAIYKLLKSHFRNEKYYIDITELFHE S.c.
68 GVGMI AINDAFLESAIYALLKKKYFRSHPAYVDMLELEFHE C.p.
68 QVGMI AINDAFMLETTSIYLLLLKKKYFRQSKHYVDLIELEFHE S.m.

170     180     190     200
155 TTFQTELGQQLCDLLTAPEDNVNLDNFSLEKYSFIV IYKTA G.f.
155 VTFQTELGQQLDLDLTAPEDSVDL SKFSLQKHSFIV IYKTA S.p.
155 VTFQTEMGQQLCDLLTEPEDKVDLDNFSMDKYTFIV IYKTA N.c.
157 VTFQTELGQQLLDLITAPEDKVDL SKFSLKHSFIV IYKTA K.l.
160 VTFQTELGQQLMDLITAPEDKVDL SKFSLKHSFIVTFKTA S.c.
108 ATFQAEELGQQLCDLITGPVDKVDLGNFSMDKYRFIV IYKTA C.s.
108 VSFQTEMGQQLCDLLTAPEDKVDLDNFSLEKYSFIV IYKTA S.m.

210     220     230     240
195 YYSFYLPVALALHQLNLATP SNL KQAEDIL IPLGEYFQIQ G.f.
195 YYSFYLPVALAMHLAGVATPENL KCAQDIL IILGKYFQVQ S.p.
195 YYSFYLPVALAMYMLD IATPENL KQAEDIL IPLGEYFQVQ N.c.
197 YYSFYLAVALAMFAAGITD SKDLKQASDVLIPLGEYFQIQ K.l.
200 YYSFYLPVALAMYVAGITDEKDLKQARDVLIPLGEYFQIQ S.c.
148 YYSFYLPVALALHQLNLATPRNLKV AEDIL IPLGEYFQVQ C.p.
148 YYSFYLPVALLLYCELA TEKNL KQAKDIL IIPMGEYFQVQ S.m.

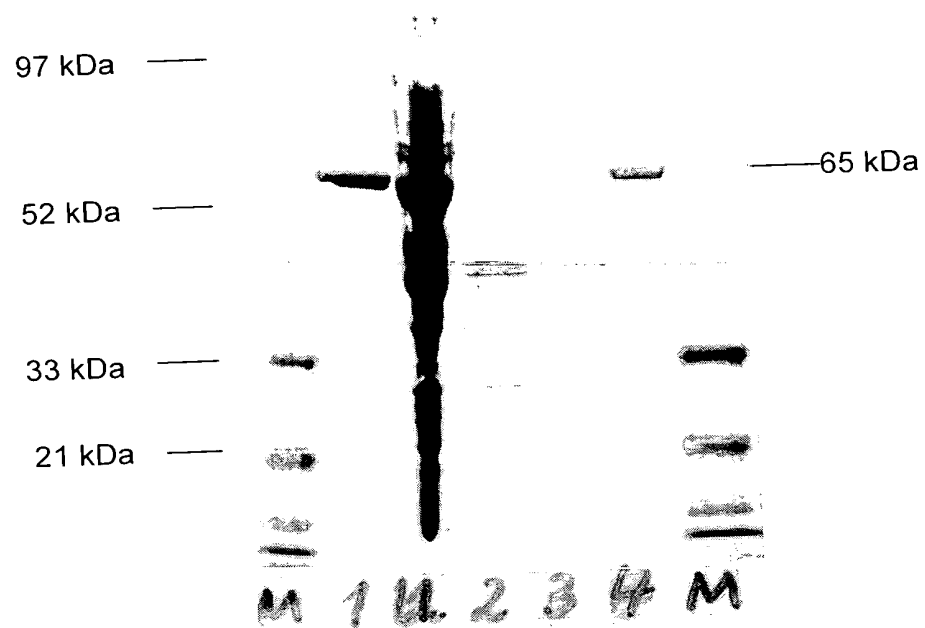
250     260     270     280
235 DDYLDNF GKPEHIGKIGTD IKDNKCSWL VNQALAVATPEQ G.f.
235 DDYLDNCF GPTVTGKIGTD ILDNKCSWI INLALAKCTPEQ S.p.
235 DDYLDNFG LPEHIGKIGTD IQDNKCSWL VNKALSI VTPEQ N.c.
237 DDFLDCFG GKPEDIGKIGTD IQDNKCSWVIN VALKNATKEQ K.l.
240 DDYLDNCF GTPEQIGKIGTD IQDNKCSWVIN KALEELASAEQ S.c.
188 DDYLDNFG RPHEHIGKIGTD IQDNK C C.p.
188 DDYLDNYADPETL GKIGTD IQGNK C S.m.

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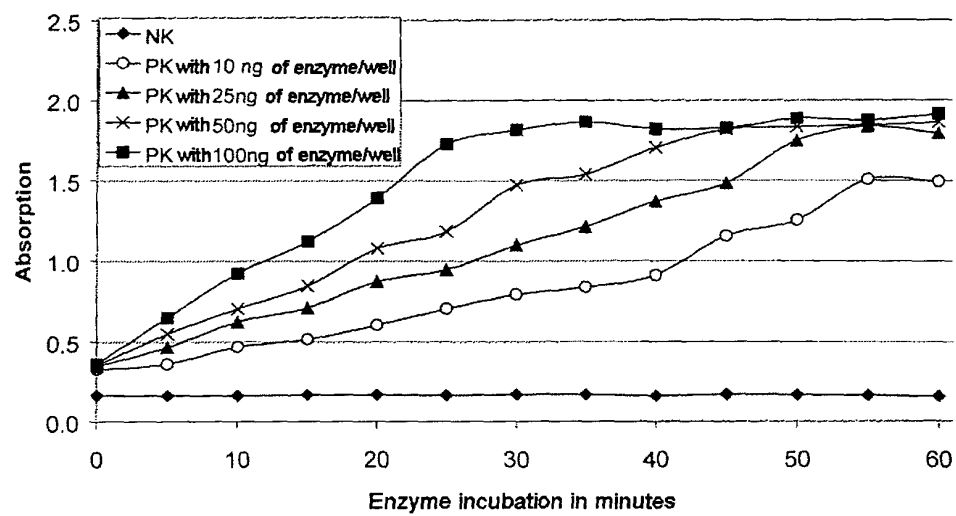
Figure 2A

	290		300		310		320
	275	R K I L E E N Y G R K D D E K E K V V K K L Y D D L N L E Q R Y L D Y E E K V V					
5		G.f.					
	275	R V I L D D N Y G R K D S E S E K R V K A V F E E L N I R G E F E N Y E E S E V					
		S.p.					
	275	R K T L E E N Y G R K D K A K E A V I K Q L Y D D L K L E D H Y K Q Y E E E R V					
		N.c.					
10	277	R D I L D E N Y G R K D S E K E Q K C R A V F N E L N I Q D I Y H K Y E E E T A					
		K.l.					
	280	R K T L D E N Y G K K D S V A E A K C K K I F N D L K I E Q L Y H E Y E E S I A					
		S.c.					
	211						
15		C.p.					
	212						
		S.m.					
			330		340		350
20	315	G Q I R E R I A N I D E N D G L K K T V F E A F L A K I Y K R S K					
		G.f.					
	315	S E I K K L I D G V D E S T G L K K S I F T T F L G K I Y K R N K					
		S.p.					
	315	G E I R K M N D A I D E S K G L K K Q V F E A F L G K I Y K R S K					
		N.c.					
25	317	S N L R E K I A N I D E S R G F K A E V L T L F L N K I Y H R K K					
		K.l.					
	320	K D L K A K I S Q V D E S R G F K A D V L T A F L N K V Y K R S K					
		S.c.					
	211						
30		C.p.					
	212						
		S.m.					

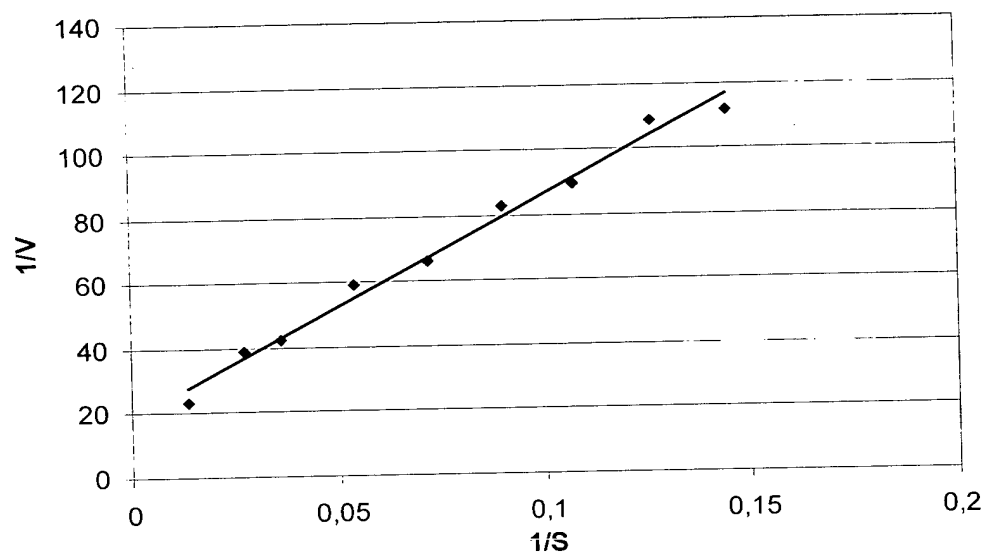
**Figure 2B**



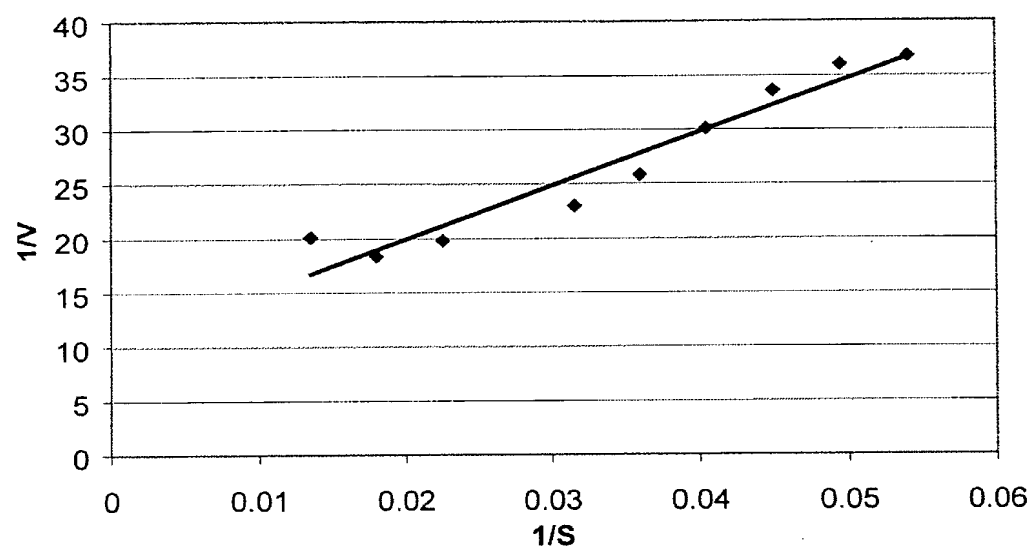
**Figure 3**



**Figure 4**



5 **Figure 5**



**Figure 6**